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RAW SEQUENCE LISTING

DATE: 12/06/2001

PATENT APPLICATION: US/09/902,188A

TIME: 11:36:38

Input Set : N:\Crf3\RULE60\09902188A.txt

Output Set: N:\CRF3\12062001\I902188A.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Bisgard-Frantzen, Henrik

6 Svendsen, Allan

7 Borchert, Torben Vedel

9 (ii) TITLE OF INVENTION: AMYLASE VARIANTS

11 (iii) NUMBER OF SEQUENCES: 32

13 (iv) CORRESPONDENCE ADDRESS:

14 (A) ADDRESSEE: Novo Nordisk of North America, Inc.

15 (B) STREET: 405 Lexington Avenue, Suite 6400

16 (C) CITY: New York

17 (D) STATE: New York

18 (E) COUNTRY: U.S.A.

19 (F) ZIP: 10174-6401

21 (v) COMPUTER READABLE FORM:

22 (A) MEDIUM TYPE: Floppy disk

23 (B) COMPUTER: IBM PC compatible

24 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

25 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

27 (vi) CURRENT APPLICATION DATA:

C--> 28 (A) APPLICATION NUMBER: US/09/902,188A

C--> 29 (B) FILING DATE: 10-Jul-2001

30 (C) CLASSIFICATION:

32 (vii) PRIOR APPLICATION DATA:

33 (A) APPLICATION NUMBER: 09/354,191

34 (B) FILING DATE:

36 (viii) ATTORNEY/AGENT INFORMATION:

37 (A) NAME: Lambiris, Elias J.

38 (B) REGISTRATION NUMBER: 33,728

39 (C) REFERENCE/DOCKET NUMBER: 4318.204-US

41 (ix) TELECOMMUNICATION INFORMATION:

42 (A) TELEPHONE: 212 867 0123

43 (B) TELEFAX: 212 867 0298

46 (2) INFORMATION FOR SEQ ID NO: 1:

48 (i) SEQUENCE CHARACTERISTICS:

49 (A) LENGTH: 485 amino acids

50 (B) TYPE: amino acid

51 (C) STRANDEDNESS: single

52 (D) TOPOLOGY: linear

54 (ii) MOLECULE TYPE: peptide

56 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

58 His His Asn Gly Thr Asn Gly Thr Met Met Gln Tyr Phe Glu Trp Tyr

59 1 5 10 15

61 Leu Pro Asn Asp Gly Asn His Trp Asn Arg Leu Arg Asp Asp Ala Ala

62 20 25 30

64 Asn Leu Lys Ser Lys Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Trp

65 35 40 45

ENTERED

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67  Lys Gly Thr Ser Gln Asn Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr
68      50                      55                      60
70  Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly
71  65                      70                      75                      80
73  Thr Arg Asn Gln Leu Gln Ala Ala Val Thr Ser Leu Lys Asn Asn Gly
74      85                      90                      95
76  Ile Gln Val Tyr Gly Asp Val Val Met Asn His Lys Gly Gly Ala Asp
77      100                     105                     110
79  Gly Thr Glu Ile Val Asn Ala Val Glu Val Asn Arg Ser Asn Arg Asn
80      115                     120                     125
82  Gln Glu Thr Ser Gly Glu Tyr Ala Ile Glu Ala Trp Thr Lys Phe Asp
83      130                     135                     140
85  Phe Pro Gly Arg Gly Asn Asn His Ser Ser Phe Lys Trp Arg Trp Tyr
86  145                     150                     155                     160
88  His Phe Asp Gly Thr Asp Trp Asp Gln Ser Arg Gln Leu Gln Asn Lys
89      165                     170                     175
91  Ile Tyr Lys Phe Arg Gly Thr Gly Lys Ala Trp Asp Trp Glu Val Asp
92      180                     185                     190
94  Thr Glu Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Val Asp Met
95      195                     200                     205
97  Asp His Pro Glu Val Ile His Glu Leu Arg Asn Trp Gly Val Trp Tyr
98      210                     215                     220
100  Thr Asn Thr Leu Asn Leu Asp Gly Phe Arg Ile Asp Ala Val Lys His
101  225                     230                     235                     240
103  Ile Lys Tyr Ser Phe Thr Arg Asp Trp Leu Thr His Val Arg Asn Thr
104      245                     250                     255
106  Thr Gly Lys Pro Met Phe Ala Val Ala Glu Phe Trp Lys Asn Asp Leu
107      260                     265                     270
109  Gly Ala Ile Glu Asn Tyr Leu Asn Lys Thr Ser Trp Asn His Ser Val
110      275                     280                     285
112  Phe Asp Val Pro Leu His Tyr Asn Leu Tyr Asn Ala Ser Asn Ser Gly
113      290                     295                     300
115  Gly Tyr Tyr Asp Met Arg Asn Ile Leu Asn Gly Ser Val Val Gln Lys
116  305                     310                     315                     320
118  His Pro Thr His Ala Val Thr Phe Val Asp Asn His Asp Ser Gln Pro
119      325                     330                     335
121  Gly Glu Ala Leu Glu Ser Phe Val Gln Gln Trp Phe Lys Pro Leu Ala
122      340                     345                     350
124  Tyr Ala Leu Val Leu Thr Arg Glu Gln Gly Tyr Pro Ser Val Phe Tyr
125      355                     360                     365
127  Gly Asp Tyr Tyr Gly Ile Pro Thr His Gly Val Pro Ala Met Lys Ser
128      370                     375                     380
130  Lys Ile Asp Pro Leu Leu Gln Ala Arg Gln Thr Phe Ala Tyr Gly Thr
131  385                     390                     395                     400
133  Gln His Asp Tyr Phe Asp His His Asp Ile Ile Gly Trp Thr Arg Glu
134      405                     410                     415
136  Gly Asn Ser Ser His Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asp
137      420                     425                     430
139  Gly Pro Gly Gly Asn Lys Trp Met Tyr Val Gly Lys Asn Lys Ala Gly

```

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```

140          435          440          445
142    Gln Val Trp Arg Asp Ile Thr Gly Asn Arg Thr Gly Thr Val Thr Ile
143          450          455          460
145    Asn Ala Asp Gly Trp Gly Asn Phe Ser Val Asn Gly Gly Ser Val Ser
146    465          470          475          480
148    Val Trp Val Lys Gln
149          485
152 (2) INFORMATION FOR SEQ ID NO: 2:
154   (i) SEQUENCE CHARACTERISTICS:
155       (A) LENGTH: 485 amino acids
156       (B) TYPE: amino acid
157       (C) STRANDEDNESS: single
158       (D) TOPOLOGY: linear
160   (ii) MOLECULE TYPE: peptide
162   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
164    His His Asn Gly Thr Asn Gly Thr Met Met Gln Tyr Phe Glu Trp His
165     1          5          10          15
167    Leu Pro Asn Asp Gly Asn His Trp Asn Arg Leu Arg Asp Asp Ala Ser
168          20          25          30
170    Asn Leu Arg Asn Arg Gly Ile Thr Ala Ile Trp Ile Pro Pro Ala Trp
171          35          40          45
173    Lys Gly Thr Ser Gln Asn Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr
174          50          55          60
176    Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly
177     65          70          75          80
179    Thr Arg Ser Gln Leu Glu Ser Ala Ile His Ala Leu Lys Asn Asn Gly
180          85          90          95
182    Val Gln Val Tyr Gly Asp Val Val Met Asn His Lys Gly Gly Ala Asp
183          100         105         110
185    Ala Thr Glu Asn Val Leu Ala Val Glu Val Asn Pro Asn Asn Arg Asn
186          115         120         125
188    Gln Glu Ile Ser Gly Asp Tyr Thr Ile Glu Ala Trp Thr Lys Phe Asp
189          130         135         140
191    Phe Pro Gly Arg Gly Asn Thr Tyr Ser Asp Phe Lys Trp Arg Trp Tyr
192     145         150         155         160
194    His Phe Asp Gly Val Asp Trp Asp Gln Ser Arg Gln Phe Gln Asn Arg
195          165         170         175
197    Ile Tyr Lys Phe Arg Gly Asp Gly Lys Ala Trp Asp Trp Glu Val Asp
198          180         185         190
200    Ser Glu Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Val Asp Met
201          195         200         205
203    Asp His Pro Glu Val Val Asn Glu Leu Arg Arg Trp Gly Glu Trp Tyr
204          210         215         220
206    Thr Asn Thr Leu Asn Leu Asp Gly Phe Arg Ile Asp Ala Val Lys His
207     225         230         235         240
209    Ile Lys Tyr Ser Phe Thr Arg Asp Trp Leu Thr His Val Arg Asn Ala
210          245         250         255
212    Thr Gly Lys Glu Met Phe Ala Val Ala Glu Phe Trp Lys Asn Asp Leu
213          260         265         270

```

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```

215 Gly Ala Leu Glu Asn Tyr Leu Asn Lys Thr Asn Trp Asn His Ser Val
216           275           280           285
218 Phe Asp Val Pro Leu His Tyr Asn Leu Tyr Asn Ala Ser Asn Ser Gly
219           290           295           300
221 Gly Asn Tyr Asp Met Ala Lys Leu Leu Asn Gly Thr Val Val Gln Lys
222           305           310           315           320
224 His Pro Met His Ala Val Thr Phe Val Asp Asn His Asp Ser Gln Pro
225           325           330           335
227 Gly Glu Ser Leu Glu Ser Phe Val Gln Glu Trp Phe Lys Pro Leu Ala
228           340           345           350
230 Tyr Ala Leu Ile Leu Thr Arg Glu Gln Gly Tyr Pro Ser Val Phe Tyr
231           355           360           365
233 Gly Asp Tyr Tyr Gly Ile Pro Thr His Ser Val Pro Ala Met Lys Ala
234           370           375           380
236 Lys Ile Asp Pro Ile Leu Glu Ala Arg Gln Asn Phe Ala Tyr Gly Thr
237           385           390           395           400
239 Gln His Asp Tyr Phe Asp His His Asn Ile Ile Gly Trp Thr Arg Glu
240           405           410           415
242 Gly Asn Thr Thr His Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asp
243           420           425           430
245 Gly Pro Gly Gly Glu Lys Trp Met Tyr Val Gly Gln Asn Lys Ala Gly
246           435           440           445
248 Gln Val Trp His Asp Ile Thr Gly Asn Lys Pro Gly Thr Val Thr Ile
249           450           455           460
251 Asn Ala Asp Gly Trp Ala Asn Phe Ser Val Asn Gly Gly Ser Val Ser
252           465           470           475           480
254 Ile Trp Val Lys Arg
255           485

```

258 (2) INFORMATION FOR SEQ ID NO: 3:

260 (i) SEQUENCE CHARACTERISTICS:

261 (A) LENGTH: 514 amino acids

262 (B) TYPE: amino acid

263 (C) STRANDEDNESS: single

264 (D) TOPOLOGY: linear

266 (ii) MOLECULE TYPE: peptide

268 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

```

270 Ala Ala Pro Phe Asn Gly Thr Met Met Gln Tyr Phe Glu Trp Tyr Leu
271 1           5           10           15
273 Pro Asp Asp Gly Thr Leu Trp Thr Lys Val Ala Asn Glu Ala Asn Asn
274           20           25           30
276 Leu Ser Ser Leu Gly Ile Thr Ala Leu Trp Leu Pro Pro Ala Tyr Lys
277           35           40           45
279 Gly Thr Ser Arg Ser Asp Val Gly Tyr Gly Val Tyr Asp Leu Tyr Asp
280           50           55           60
282 Leu Gly Glu Phe Asn Gln Lys Gly Ala Val Arg Thr Lys Tyr Gly Thr
283           65           70           75           80
285 Lys Ala Gln Tyr Leu Gln Ala Ile Gln Ala Ala His Ala Ala Gly Met
286           85           90           95
288 Gln Val Tyr Ala Asp Val Val Phe Asp His Lys Gly Gly Ala Asp Gly

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289		100		105		110													
291	Thr	Glu	Trp	Val	Asp	Ala	Val	Glu	Val	Asn	Pro	Ser	Asp	Arg	Asn	Gln			
292			115					120					125						
294	Glu	Ile	Ser	Gly	Thr	Tyr	Gln	Ile	Gln	Ala	Trp	Thr	Lys	Phe	Asp	Phe			
295			130				135						140						
297	Pro	Gly	Arg	Gly	Asn	Thr	Tyr	Ser	Ser	Phe	Lys	Trp	Arg	Trp	Tyr	His			
298			145			150						155				160			
300	Phe	Asp	Gly	Val	Asp	Trp	Asp	Glu	Ser	Arg	Lys	Leu	Ser	Arg	Ile	Tyr			
301				165						170					175				
303	Lys	Phe	Arg	Gly	Ile	Gly	Lys	Ala	Trp	Asp	Trp	Glu	Val	Asp	Thr	Glu			
304				180					185					190					
306	Asn	Gly	Asn	Tyr	Asp	Tyr	Leu	Met	Tyr	Ala	Asp	Leu	Asp	Met	Asp	His			
307			195					200					205						
309	Pro	Glu	Val	Val	Thr	Glu	Leu	Lys	Ser	Trp	Gly	Lys	Trp	Tyr	Val	Asn			
310			210				215					220							
312	Thr	Thr	Asn	Ile	Asp	Gly	Phe	Arg	Leu	Asp	Ala	Val	Lys	His	Ile	Lys			
313			225			230					235				240				
315	Phe	Ser	Phe	Phe	Pro	Asp	Trp	Leu	Ser	Asp	Val	Arg	Ser	Gln	Thr	Gly			
316				245						250				255					
318	Lys	Pro	Leu	Phe	Thr	Val	Gly	Glu	Tyr	Trp	Ser	Tyr	Asp	Ile	Asn	Lys			
319				260					265					270					
321	Leu	His	Asn	Tyr	Ile	Met	Lys	Thr	Asn	Gly	Thr	Met	Ser	Leu	Phe	Asp			
322			275					280					285						
324	Ala	Pro	Leu	His	Asn	Lys	Phe	Tyr	Thr	Ala	Ser	Lys	Ser	Gly	Gly	Thr			
325			290				295					300							
327	Phe	Asp	Met	Arg	Thr	Leu	Met	Thr	Asn	Thr	Leu	Met	Lys	Asp	Gln	Pro			
328			305			310					315				320				
330	Thr	Leu	Ala	Val	Thr	Phe	Val	Asp	Asn	His	Asp	Thr	Glu	Pro	Gly	Gln			
331				325						330				335					
333	Ala	Leu	Gln	Ser	Trp	Val	Asp	Pro	Trp	Phe	Lys	Pro	Leu	Ala	Tyr	Ala			
334				340					345					350					
336	Phe	Ile	Leu	Thr	Arg	Gln	Glu	Gly	Tyr	Pro	Cys	Val	Phe	Tyr	Gly	Asp			
337			355				360					365							
339	Tyr	Tyr	Gly	Ile	Pro	Gln	Tyr	Asn	Ile	Pro	Ser	Leu	Lys	Ser	Lys	Ile			
340			370				375					380							
342	Asp	Pro	Leu	Leu	Ile	Ala	Arg	Arg	Asp	Tyr	Ala	Tyr	Gly	Thr	Gln	His			
343			385			390					395				400				
345	Asp	Tyr	Leu	Asp	His	Ser	Asp	Ile	Ile	Gly	Trp	Thr	Arg	Glu	Gly	Val			
346				405					410					415					
348	Thr	Glu	Lys	Pro	Gly	Ser	Gly	Leu	Ala	Ala	Leu	Ile	Thr	Asp	Gly	Pro			
349				420					425					430					
351	Gly	Gly	Ser	Lys	Trp	Met	Tyr	Val	Gly	Lys	Gln	His	Ala	Gly	Lys	Val			
352			435				440					445							
354	Phe	Tyr	Asp	Leu	Thr	Gly	Asn	Arg	Ser	Asp	Thr	Val	Thr	Ile	Asn	Ser			
355			450				455					460							
357	Asp	Gly	Trp	Gly	Glu	Phe	Lys	Val	Asn	Gly	Gly	Ser	Val	Ser	Val	Trp			
358			465			470					475				480				
360	Val	Pro	Arg	Lys	Thr	Thr	Val	Ser	Thr	Ile	Ala	Trp	Ser	Ile	Thr	Thr			
361				485					490					495					

VERIFICATION SUMMARY

DATE: 12/06/2001

PATENT APPLICATION: US/09/902,188A

TIME: 11:36:40

Input Set : N:\Crf3\RULE60\09902188A.txt

Output Set: N:\CRF3\12062001\I902188A.raw

L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]